

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bander, Neil H.
- (ii) TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 - (B) STREET: Clinton Square, P.O. Box 1051
 - (C) CITY: Rochester
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 14603-1051
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/016,976
 - (B) FILING DATE: 06-MAY-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 06/022,125
 - (B) FILING DATE: 18-JUL-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Goldman, Michael L.
 - (B) REGISTRATION NUMBER: 30,727
 - (C) REFERENCE/DOCKET NUMBER: 19603/1172
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (716) 263-1304
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCTCCTGTCA GGA	ACTGCAG	GTGTCCTCTC	TGAGGTCCAG	CTGCAACAGT	CTGGACCTGA	60
ACTGGTGAAG	CCTGGGACTT	CAGTGAGGAT	ATCCTGCAAG	ACTTCTGGAT	ACACATTCAC	120
TGAATATACC	ATACACTGGG	TGAAGCAGAG	CCATGGAAAAG	AGCCTTGAGT	GGATTGGAAA	180
CATCAATCCT	AACAATGGTG	GTACCACCTA	CAATCAGAAG	TTCGAGGACA	AGGCCACATT	240
GACTGTAGAC	AAGTCCTCCA	GTACAGCCTA	CATGGAGCTC	CGCAGCCTAA	CATCTGAGGA	300
TTCTGCAGTC	TATTATTGTG	CAGCTGTTG	GAACTTTGAC	TACTGGGGCC	AAGGCACCAC	360
TCTCACAGTC	TCCTCAGCCA	AAACGACACC	C			391

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGTGTCGTT	TTGGCTGAGG	AGACTGTGAG	AGTGGTGCCT	TGGCCCCAGT	AGTCAAAGTT	60
CCAACCAGCT	GCACAATAAT	AGACTGCAGA	ATCCTCAGAT	GTTAGGCTGC	GGAGCTCCAT	120
GTAGGCTGTA	CTGGAGGACT	TGTCTACAGT	CAATGTGGCC	TTGTCTCGA	ACTTCTGATT	180
GTAGGTGGTA	CCACCATGTG	TAGGATTGAT	GTTTCCAATC	CACTCAAGGC	TCTTTCCATG	240
GCTCTGCTTC	ACCCAGTGTA	TGGTATATTC	AGTGAATGTG	TATCCAGAAG	TCTTGCAGGA	300
TATCTCACT	GAAGTCCCAG	GCTTCACCAG	TTCAGGTCCA	GACTGTTGCA	GCTGGACCTC	360
AGAGAGGACA	CCTGCAGTTC	CTAGCAGGAG	A			391

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser	Pro	Val	Arg	Asn	Cys	Arg	Cys	Pro	Leu	Gly	Pro	Ala	Ala	Thr	Val	1	5	10	15
Trp	Thr	Thr	Gly	Glu	Ala	Trp	Asp	Phe	Ser	Glu	Asp	Ile	Leu	Gln	Asp	20	25	30	
Phe	Trp	Ile	His	Ile	His	Ile	Tyr	His	Thr	Leu	Gly	Glu	Ala	Glu	Pro	35	40	45	
Trp	Lys	Glu	Pro	Val	Asp	Trp	Lys	His	Gln	Ser	Gln	Trp	Trp	Tyr	His	50	55	60	
Leu	Gln	Ser	Glu	Val	Arg	Gly	Gln	Gly	His	Ile	Asp	Cys	Arg	Gln	Val	65	70	75	
Leu	Gln	Tyr	Ser	Leu	His	Gly	Ala	Pro	Gln	Pro	Asn	Ile	Gly	Phe	Cys	85	90	95	
Ser	Leu	Leu	Leu	Cys	Ser	Trp	Leu	Glu	Leu	Leu	Leu	Gly	Pro	Arg	His	100	105	110	
His	Ser	His	Ser	Leu	Leu	Ser	Gln	Asn	Asp	Thr	115	120							

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu	Leu	Ser	Gly	Thr	Ala	Gly	Val	Leu	Ser	Glu	Val	Gln	Leu	Gln	Gln	1	5	10	15
Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Thr	Ser	Val	Arg	Ile	Ser	Cys	20	25	30	
Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Glu	Tyr	Thr	Ile	His	Trp	Val	Lys	35	40	45	

Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Asn Ile Asn Pro Asn
50 55 60
Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe Glu Asp Lys Ala Thr Leu
65 70 75 80
Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu
85 90 95
Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Ala Gly Trp Asn Phe
100 105 110
Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
115 120 125
Thr Pro
130

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Leu Ser Cys Gln Glu Leu Gln Val Ser Ser Leu Arg Ser Ser Cys Asn
1 5 10 15
Ser Leu Asp Leu Asn Trp Ser Leu Gly Leu Gln Gly Tyr Pro Ala Arg
20 25 30
Leu Leu Asp Thr His Ser Leu Asn Ile Pro Tyr Thr Gly Ser Arg Ala
35 40 45
Met Glu Arg Ala Leu Ser Gly Leu Glu Thr Ser Ile Leu Thr Met Val
50 55 60
Val Pro Pro Thr Ile Arg Ser Ser Arg Thr Arg Pro His Leu Thr Ser
65 70 75 80
Pro Pro Val Gln Pro Thr Trp Ser Ser Ala Ala His Leu Arg Ile Leu
85 90 95
Gln Ser Ile Ile Val Gln Leu Val Gly Thr Leu Thr Thr Gly Ala Lys
100 105 110
Ala Pro Leu Ser Gln Pro Ser Gln Pro Lys Arg His Pro
115 120 125

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAGGTCACGC TGCAACAGTC TGGACCTGAA CTGGTGAAGC CTGGGACTTC AGTGAGGATA	60
TCCTGCAAGA CTTCTGATA CACATTCCT GAATATACCA TACACTGGGT GAAGCAGAGC	120
CATGGAAAGA GCCTTGAGTG GATTGGAAAC ATCAATCCTA ACAATGGTGG TACCACCTAC	180
AATCAGAAGT TCGAGGACAA GGCCACATTG ACTGTAGACA AGTCCTCCAG TACAGCCTAC	240
ATGGAGCTCC GCAGCCTAAC ATCTGAGGAT TCTGCAGTCT ATTATTGTGC AGCTGGTTGG	300
AACTTTGA CTCTGGGGCCA AGGCACCACT CTCACAGTCT CCTCA	345

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGAGGAGACT GTGAGAGTGG TGCCTTGGCC CCAGTAGTCA AAGTTCCAAC CAGCTGCACA	60
ATAATAGACT GCAGAATCCT CAGATGTTAG GCTGCGGAGC TCCATGTAGG CTGTACTGGA	120
GGACTTGTCT ACAGTCAATG TGGCCTTGTC CTCGAACTTC TGATTGTAGG TGGTACCACC	180
ATTGTTAGGA TTGATGTTTC CAATCCACTC AAGGCTCTTT CCATGGCTCT GCTTCACCCA	240
GTGTATGGTA TATTCAGTGA ATGTGTATCC AGAAGTCTTG CAGGATATCC TCACTGAAGT	300
CCCAGGCTTC ACCAGTTCAG GTCCAGACTG TTGCAGCTGG ACCTC	345

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Thr
 1 5 10 15
 Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
 20 25 30
 Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45
 Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe
 50 55 60
 Glu Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
 100 105 110
 Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTATATGGAG CTGATGGGAA CATTGTAATG ACCCAATCTC CCAAATCCAT GTCCATGTCA 60
 GTAGGAGAGA GGGTCACCTT GACCTGCAAG GCCAGTGAGA ATGTGGTTAC TTATGTTTCC 120
 TGGTATCAAC AGAAACCAGA GCAGTCTCCT AAAGTCTGTA TATACGGGGC ATCCAACCGG 180
 TACTACTGGGG TCCCCGATCG CTTACAGGC AGTGGATCTG CAACAGATT TACTCTGACC 240

ATCAGCAGTG TGCAGGCTGA AGACCTTGCA GATTATCACT GTGGACAGGG TTACAGCTAT	300
CCGTACACGT TCGGAGGGGG GACCAAGCTG GAAATAAAAC GGGCTGATGC TGCACCAACT	360
GTA	363

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TACAGTTGGT GCAGCATCAG CCCGTTTTAT TTCCAGCTTG GTCCCCCTC CGAACGTGTA	60
CGGATAGCTG TAACCTGTG CACAGTGATA ATCTGCAAGG TCTTCAGCCT GCACACTGCT	120
GATGGTCAGA GTGAAATCTG TTGCAGATCC ACTGCCTGTG AAGCGATCGG GGACCCCACT	180
GTACCGGTTG GATGCCCCGT ATATCAGCAG TTTAGGAGAC TGCTCTGGTT TCTGTGATA	240
CCAGGAAACA TAAGTAACCA CATTCTCACT GGCCTTGAG GTCAAGGTGA CCCTCTCTCC	300
TACTGACATG GACATGGATT TGGGAGATTG GGTCAATACA ATGTTCCCAT CAGCTCCATA	360
TAA	363

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Leu Tyr Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser	
1 5 10 15	
Met Ser Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys Lys Ala Ser	
20 25 30	
Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln	
35 40 45	
Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val	
50 55 60	

Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln
85 90 95
Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile
100 105 110
Lys Arg Ala Asp Ala Ala Pro Thr Val
115 120

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr Met Glu Leu Met Gly Thr Leu Pro Asn Leu Pro Asn Pro Cys Pro
1 5 10 15
Cys Gln Glu Arg Gly Ser Pro Pro Ala Arg Pro Val Arg Met Trp Leu
20 25 30
Leu Met Phe Pro Gly Ile Asn Arg Asn Gln Ser Ser Leu Leu Asn Cys
35 40 45
Tyr Thr Gly His Pro Thr Gly Thr Leu Gly Ser Pro Ile Ala Ser Gln
50 55 60
Ala Val Asp Leu Gln Gln Ile Ser Leu Pro Ser Ala Val Cys Arg Leu
65 70 75 80
Lys Thr Leu Gln Ile Ile Thr Val Asp Arg Val Thr Ala Ile Arg Thr
85 90 95
Arg Ser Glu Gly Gly Pro Ser Trp Lys Asn Gly Leu Met Leu His Gln
100 105 110
Leu Tyr

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile Ile Trp Ser Trp Glu His Cys Asn Asp Pro Ile Ser Gln Ile His
 1 5 10 15
 Val His Val Ser Arg Arg Glu Gly His Leu Asp Leu Gln Gly Gln Glu
 20 25 30
 Cys Gly Tyr Leu Cys Phe Leu Val Ser Thr Glu Thr Arg Ala Val Ser
 35 40 45
 Thr Ala Asp Ile Arg Gly Ile Gln Pro Val His Trp Gly Pro Arg Ser
 50 55 60
 Leu His Arg Gln Trp Ile Cys Asn Arg Phe His Ser Asp His Gln Gln
 65 70 75 80
 Cys Ala Gly Arg Pro Cys Arg Leu Ser Leu Trp Thr Gly Leu Gln Leu
 85 90 95
 Ser Val His Val Arg Arg Gly Asp Gln Ala Gly Asn Lys Thr Gly Cys
 100 105 110
 Cys Thr Asn Cys
 115

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AACATTGTAA TGACCCAATC TCCCAAATCC ATGTCCATGT CAGTAGGAGA GAGGGTCACC	60
TTGACCTGCA AGGCCAGTGA GAATGTGGTT ACTTATGTTT CCTGGTATCA ACAGAAACCA	120
GAGCAGTCTC CTAAACTGCT GATATACGGG GCATCCAACC GGTACACTGG GGTCCCGAT	180
CGCTTCACAG GCAGTGGATC TGCAACAGAT TTTCACTCTGA CCATCAGCAG TGTGCAGGCT	240
GAAGACCTTG CAGATTATCA CTGTGGACAG GGTACAGCT ATCCGTACAC GTTCGGAGGG	300
GGGACCAAGC TGGAAATAAA A	321

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTTATTTC AGCTTGGTCC CCCCTCCGAA CGTGACGGA TAGCTGTAAC CCTGTCCACA 60
 GTGATAATCT GCAAGGTCTT CAGCCTGCAC ACTGCTGATG GTCAGAGTGA AATCTGTTGC 120
 AGATCCACTG CCTGTGAAGC GATCGGGGAC CCCAGTGTAC CGGTTGGATG CCCC GTATAT 180
 CAGCAGTTTA GGAGACTGCT CTGTTTCTG TTGATACCAG GAAACATAAG TAACCACATT 240
 CTCCTGGGCC TTGCAGGTCA AGGTGACCCT CTCTCCTACT GACATGGACA TGGATTGGG 300
 AGATTGGGTC ATTACAATGT T 321

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
 1 5 10 15
 Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr
 20 25 30
 Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile
 35 40 45
 Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60
 Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala
 65 70 75 80
 Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACATTGTGA TGACCCAGTC TCACAAATTC ATGTCCACAT CAGTAGGAGA CAGGGTCAGC 60
ATCATCTGTA AGGCCAGTCA AGATGTGGGT ACTGCTGTAG ACTGGTATCA ACAGAAACCA 120
GGACAATCTC CTAAACTACT GATTTATTGG GCATCCACTC GGCACACTGG AGTCCCTGAT 180
CGCTTCACAG GCAGTGGATC TGGGACAGAC TTCACTCTCA CCATTACTAA TGTTCAGTCT 240
GAAGACTTGG CAGATTATTT CTGTCAGCAA TATAACAGCT ATCCTCTCAC GTTCGGTGCT 300
GGGACCATGC TGGACCTGAA A 321

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTCAGGTCC AGCATGGTCC CAGCACCGAA CGTGAGAGGA TAGCTGTTAT ATTGCTGACA 60
GAAATAATCT GCCAAGTCTT CAGACTGAAC ATTAGTAATG GTGAGAGTGA AGTCTGTCCC 120
AGATCCACTG CCTGTGAAGC GATCAGGGAC TCCAGTGTGC CGAGTGGATG CCCAATAAAT 180
CAGTAGTTTA GGAGATTGTC CTGGTTTCTG TTGATACCAG TCTACAGCAG TACCCACATC 240
TTGACTGGCC TTACAGATGA TGCTGACCCT GTCTCCTACT GATGTGGACA TGAATTGTG 300
AGACTGGGTC ATCACAATGT C 321

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15
Asp Arg Val Ser Ile Ile Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
20 25 30
Val Asp Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45
Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser
65 70 75 80
Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95
Thr Phe Gly Ala Gly Thr Met Leu Asp Leu Lys
100 105